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Genetic divergence studies in clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.]

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ABSTRACT: The present investigation was carried out in Randomized Block Design with four replications on thirty genotypes of cluster bean to assess genetic divergence using the Mahalanobis D^2 technique. Gum content in seed contributed the maximum to the total divergence followed by days to flowering, number of pods per plant, days to maturity and protein content. Genotypes were grouped into 5 clusters using Tocher's method. Cluster II was the largest group (11 genotypes) followed by cluster I (10 genotypes) and seven genotypes in cluster III. The remaining solitary clusters (IV and V) contained only one genotype each. Based on inter-cluster distance and performance observed in the present study intercross between the genotype of clusters II (GG 1908, GG 1911, GG 2102, GG 2104, GG 1906, GG 1912, GG 1907, GG 1909, GG 1904, GG 2103) and cluster IV (GG 2111) would be effective for improving seed yield in clusterbean.

Keywords: Genotypes, Genetic divergence, inter-cluster distance, Cluster bean.

INTRODUCTION

Clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] (2n=2x=14) is an underexploited legume belonging to the family *Fabaceae*. It is a short-day self-pollinated crop (Undersander *et al*., 1991), commonly known as guar, chavlikayi, guari and khutti etc. The word "guar" represents a derivation from the Sanskrit word "Gaaahar" which means cow food or fodder of livestock (Bhosle and Kothekar 2010). It is a versatile legume crop cultivated mostly as animal feed, green manure (Chudzikowski, 1971 and Siddaraju *et al*., 2010), green leaves as fodder, vegetable and cover crop (Arora and Pahuja, 2008). Clusterbean is grown mainly in the *Kharif* season. It is a photosensitive crop and requires a specific climatic condition to grow for proper germination. Due to high drought and salinity tolerance (Francois *et al*., 1990) and (Ashraf *et al*., 2005), guar could be a valuable alternative crop for the exploitation of semi-arid environments. It grows best in sandy soils, with a rainfall range of 250 to 450 mm and a temperature range of 25°C to 40°C. The optimum pH value is between 7 to 8, guar enhances soil productiveness by fixing atmospheric nitrogen for its necessity and also for the succeeding crop (Bewal *et al*., 2009).

Gillette (1958) divided the genus *Cyamopsis* into three races, *viz*., *Cyamopsis tetragonoloba* (L.) Taub, *Cyamopsis senegalensis* Guill. and Perr. and *Cyamopsis serrata* Schinz. The haploid and diploid chromosome numbers of all three genus species of *Cyamopsis* were reported to be n = 7 and 2n = 14. Gillete (1958) suggested that the most probable origin of clusterbean in Africa is due to the presence of many wild relatives in Africa. *C. tetragonoloba* seeds are almost round. At maturity, *C. senegalensis* and *C. serrata* also exhibit pod shattering, although *C. tetragonoloba* does not (Menon, 1973). From the outside to the inside of the dicotyledonous seed of the clusterbean, three primary portions are present: the husk or hull (14–17%), the endosperm (35–42%), and the germ or embryo (43–47 percent). In contrast to most other legumes, the clusterbean seed has a very big endosperm. When processing clusterbean seeds for gum, dull-white, wrinkle-free seeds are desirable; black seeds are said to provide inferior gum (Bhatia *et al*., 1979; Hymowitz and Matlock 1963).

In India, guar is being grown mainly in arid and semi-arid regions of North-Western states of Rajasthan, Gujarat, Haryana, Punjab, parts of Uttar Pradesh, Madhya Pradesh and Tamil Nadu.

Rajasthan occupies the largest area under guar cultivation (82.1%), followed by Haryana (8.6%), Gujarat (8.3%) and Punjab (1%) which in turn produced 64, 22, 12 and 2 percent guar seeds, respectively (Pathak *et al*., 2010). In, Gujarat is mainly grown in Banashkantha, Mahesana, Ahmedabad, Anand, Kheda, Gandhinagar, and Kutch districts. The cultivated area under guar in Gujarat was 1.23 lakh ha with a production of 0.86 lakh tonnes and productivity of 699.4 kg/ha (Anonymous, 2021).

The genetic resources of guar have been employed to raise agricultural yield potential, broaden adaption, develop tolerance to disease, and pest stress, and improve quality and stature. The main genetic support for the crops comes from their wild relatives, who also assist in preserving their prized status. Superior genotypes of clusterbean have been released as a result of the choices made through local landraces (Henry *et al*., 1992; Bharodia *et al*., 1993; Mishra *et al*., 2009). Branched or unbranched plant types, hairy or smooth stems, straight or sickle-shaped pods, pubescent or glabrous leaves, determinate or indeterminate development, and regular or irregular pod-bearing behaviors are only a few of the many variations in the known clusterbean germplasm (Saini *et al*., 1981). According to Ogwu *et al*. (2014), one of the most sustainable ways to preserve priceless genetic resources while simultaneously increasing agricultural output and food security are to use a variety of germplasms to improve crops. For this reason, the present study was carried out to evaluate genetic diversity in this priceless legume crop.

MATERIALS AND METHOD

The present investigation was carried out with thirty diverse clusterbean genotypes (Table 1) received from Pulses Research Station, Sardarkrushinagarand evaluated with four replications in Randomized Block Design (RBD) during *Kharif* 2020-21 at Agronomy Instructional Farm, S. D. Agricultural University, Sardarkrushinagar, Gujrat. The center is situated 24˚-19'North latitude and 72˚-19' East latitude with an elevation of 154.52 meters above mean sea level and represents the North Gujarat Agro-climatic region. The general view of the experimental site is depicted in (Fig. 1). Climatic conditions during the experimental period at present in Table 2 and Fig. 2. Observations from five randomly selected plants of each genotype in each replication were recorded on nine quantitative [days to flowering, plant height (cm), number of branches per plant, number of pod per plant, pod length (cm), days to maturity, number of seed per pod, test weight (g) and seed yield per plant (g)] and two biochemical characters [gum content (%) and protein content (%)]. Each genotype was represented by a single row of 4.0 m in length. The inter and intra-row distances were 45 cm and 15 cm, respectively. The mean performance of each genotype for all traits was subjected to statistical analysis. The analysis was carried out by the Mahalanobis D^2 technique (Mahalanobis, 1936). The genotypes were grouped into different clusters following Tocher's method as described by Rao (1952).

Table 1: List of genotypes used in the present study.

Sr. No.	Genotypes	Sr. No.	Genotypes	Sr. No.	Genotypes
1.	GG 1	11.	GG 1908	1.	G 2105
2.	GG 2	12.	GG 1909	2.	G 2106
3.	GAUG 1305	13.	GG 1910	3.	G 2107
4.	GG 1901	14.	GG 1911	4.	G 2108
5.	GG 1902	15.	GG 1912	5.	G 2109
6.	GG 1903	16.	GG 1913	6.	G 2110
7.	GG 1904	17.	GG 2101	7.	G 2111
8.	GG 1905	18.	GG 2102	8.	G 2112
9.	GG 1906	19.	GG 2103	9.	G 2113
10.	GG 1907	20.	GG 2104	10.	G 2114

Note: All the genotypes were collected from Pulses Research Station Sardarkrushinagar

Fig. 1. General view of the experimental site.

Table 2: Meteorological data during the crop season (July -2021 to October 2021).

Month and year	Std. Weeks	Temperature (°C)		Relative Humidity (%)		Rainfall (mm)
		Max.	Min.	Morn.	Even.	
Month and year	26	37.2	25.6	79	65	9.0
	27	38.0	26.8	76	65	0.0
	28	39.1	26.0	81	63	47.0
	29	36.1	26.2	82	75	8.0
	30	31.6	24.8	85	90	65.5
	31	29.0	24.3	84	85	17.5
August 2021	32	33.5	25.9	80	74	0.0
	33	36.5	25.7	73	68	0.0
	34	36.9	26.0	76	67	2.0
	35	35.6	24.7	82	66	36.5
September 2021	36	34.4	24.9	88	83	41.0
	37	32.9	24.2	85	83	109.5
	38	33.5	23.6	80	77	6.0
	39	33.1	24.9	81	77	87.5
October 2021	40	34.7	25.0	78	70	0.0
	41	37.4	25.8	77	62	0.0
	42	36.9	21.1	69	62	0.0
	43	36.2	18.0	66	59	0.0
	44	33.3	15.9	69	50	0.0

Source: Agricultural Meteorology Department, C. P. College of Agriculture, Sardarkrushinagar

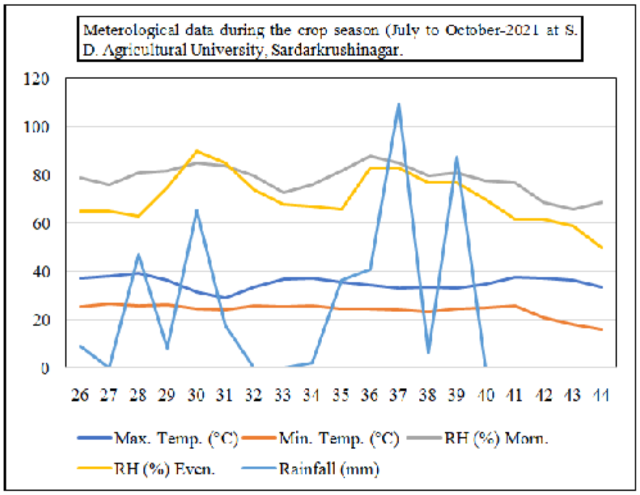

Fig. 2. Meteorological data during the crop season.

RESULTS AND DISCUSSION

The foundational element for a successful breeding program is genetic diversity. Any program must include the collection and evaluation of germplasm lines and genotypes of every crop, which increases the potential for utilizing genetic diversity. The Mahalanobis D^2 method (Mahalanobis, 1936) is a potent instrument for calculating the genetic divergence among a group of genotypes.

A. Distribution of genotypes evaluated for seed yield into different clusters

Tocher's approach (Rao, 1952) was used to group the genotypes, with the underlying premise that genotypes within a cluster had lower D^2 values among themselves than those from groups belonging to other clusters. From 30 genotypes, five clusters all emerged. Table 3, displays the genotype distributions into five groupings. With eleven genotypes, Cluster II was the largest cluster, followed by Cluster I, which had ten genotypes. Clusters IV and V each have one genotype, while Cluster III has seven genotypes. Remzeena *et al*. (2018) noted a comparable genotype distribution.

B. Average Intra and inter-cluster D^2 value

Intra cluster average D^2 values ranged from 0.00 to 113.21 (Table 4). Among the clusters, cluster II had the maximum intra-cluster distance ($D^2 = 113.21$), followed by cluster III ($D^2 = 109.96$) and cluster I ($D^2 = 109.49$). The zero intra-clusters distance was observed for clusters IV and V ($D^2 = 0.00$).

Table 3: Distribution of genotypes evaluated for seed yield in different clusters.

Cluster	No. of genotypes	Name of the genotypes
I	10	GG 2108, GG 2113, GG 2107, GG 2114, GG 2109, GG 1910, GG 2106, GG 2110, GG 2101, GG 2112
II	11	GG 1908, GG 1911, GG 2102, GG 2104, GG 1906, GG 1912, GG 1907, GG 1909, GG 1904, GG 2105, GG 2103
III	7	GG 2, GG 1902, GG 1903, GG 1901, GG 1905, GAUG 1305, GG 1
IV	1	GG 2111
V	1	GG 1913

The maximum inter-cluster distance was recorded between cluster II and cluster IV (D^2 = 558.37) followed by that between III and IV (D^2 = 494.20), while the minimum inter-cluster distance was observed between clusters I and IV (D^2 = 209.26). Inter-cluster distances were higher than intra-cluster distances which indicated the existence of substantial diversity among the genotypes. The selection of parents for crossing from divergent clusters may result in heterotic expression for yield and quality traits. Similar observations were recorded by Kumar *et al*. (2014).

C. Cluster means seed yield and its components traits

The mean performance of clusters for eleven characters is presented in (Table 5). Cluster III had the highest cluster mean for days to flowering (46.79), days to maturity (101.04) and plant height (40.83). Cluster IV had the highest cluster mean for the number of branches per plant (5.10), gum content (28.23) and protein content (26.68). Cluster V had the highest cluster mean for the number of pods per plant (39.50), pod length (5.20), test weight (2.99) and seed yield per plant (7.43). Similar observations were recorded by Kumar *et al*. (2014).

D. The relative contribution of different characters toward genetic diversity

The components of D^2 due to each character variable were ranked ascending to the highest value. The total of these ranks over all possible [n (n − 1)/2] = 435 combinations would provide indirect information about the order of priority in terms of the percentage contribution of the character to the total divergence. These percentages are presented in (Table 6).

Among all the characters, gum content (42.30 %) contributed the maximum to the diversity by taking the first rank 184 times out of 435 combinations, followed by days to flowering (28.28 %) with 123 times, the number of pods per plant (13.33 %) with 58 times, days to maturity (7.82 %) with 34 times. While, protein content (4.14 %) with 18-time, number of branches per plant (3.45) 15 times, number of seeds per pod (0.23 %) with one time, test weight (0.23 %) with one time and plant height (0.23 %) with one time. While characters like the pod length and seed yield per plant contributed null towards the total genetic divergence.

In the present study, gum content (42.30 %), days to flowering (28.28 %) and the number of pods per plant (13.33 %) were the main contributors to the total divergence. These traits may play important role in germplasm collection and evaluation. Remzeena *et al*. (2018) also observed high diversity for days to flowering and moderate to low contribution towards the total divergence, for days to maturity, protein content, number of branches per plant, plant height, number of seeds per pod and test weight; Shekhawat and Choudhary (2004) for days to flowering and Wankhade *et al*. (2017) for gum content.

Table 4: Average intra and inter-cluster D^2 value.

	I	II	III	IV	V
I	**109.4932**	219.1678	340.3358	209.2579	376.6327
II	-	**113.2132**	327.6290	558.3730	342.7630
III	-	-	**109.9630**	494.2092	393.6954
IV	-	-	-	**0.0000**	447.7004
V	-	-	-	-	**0.0000**

Table 5: Cluster means for seed yield and its components in clusterbean.

Cluster	DF	DM	PH	NBPP	NPPP	PL	NSPP	TW	GC	PC	SYPP
I	28.45	70.25	46.77	4.79	15.74	4.95	6.96	2.59	23.57	26.60	2.99
II	28.89	84.86	43.59	4.91	16.50	4.91	6.19	2.56	19.64	26.67	2.85
III	46.79	101.04	40.83	4.93	11.92	5.02	6.36	2.66	23.04	26.62	2.34
IV	26.00	64.00	49.50	5.10	24.80	4.70	6.70	2.50	28.23	26.68	3.99
V	35.00	84.50	45.20	3.80	39.50	5.20	6.40	2.99	21.18	26.02	7.43

Where,

DF= Days to flowering, DM = Days to maturity, PH= Plant height (cm), NBPP= Number of branch per plant, NPPP= Number of pod per plant, PL= Pod length (cm), NSPP= Number of seed per pod, TW= Test weight (g), GC= Gum content (%), PC= Protein content (%), SYPP= Seed yield per plant (g)

Table 6: Relative contribution of different characters towards genetic diversity evaluated for seed yield.

Sr. No.	Characters	Time ranked 1st	Contribution to divergence (%)
1.	Days to flowering	123	28.28
2.	Days to maturity	34	7.82
3.	Plant height (cm)	1	0.23
4.	Number of branch per plant	15	3.45
5.	Number of pod per plant	58	13.33
6.	Pod length (cm)	0	0
7.	Number of seed per pod	1	0.23
8.	Test weight (g)	1	0.23
9.	Gum content (%)	184	42.30
10.	Protein content (%)	18	4.14
11.	Seed yield per plant (g)	0	0

CONCLUSION

In the present investigation, the 30 genotypes were grouped into 5 clusters. Cluster II had the maximum intra-cluster distance, while the minimum intra-cluster distance was observed for cluster IV. The maximum inter-cluster distance was recorded between cluster II and cluster IV, while the minimum inter-cluster distance was observed between clusters I and IV. The intercluster distance was higher than intra cluster distance indicating the presence of substantial genetic diversity. Whereas, intercross of the genotype clusters II (GG 1908, GG 1911, GG 2102, GG 2104, GG 1906, GG 1912, GG 1907, GG 1909, GG 1904, GG 2105, GG 2103) and cluster IV (GG 2111) would be effective for creating a wide spectrum of variability and improving seed yield in clusterbean. Cluster III had the highest mean values for the number of days to flowering, plant height and maturity. Cluster IV had a desirable high rating for the number of branches per plant, gum content and protein content. Cluster V had a desirable high rating for the number of pods per plant, pod length, test weight and seed yield per plant. The data clearly show that character-wise contribution varies throughout clusters, thus if a single character needs to be improved, it can be done by using genotypes from the cluster that has the highest mean values for that character. The cross combinations that may produce the maximum variability for certain qualities are thus determined by the clustering pattern. Cluster means and inter-cluster distance can also be used to choose the best genotypes for the breeding program. Gum content, days to blooming, and the number of pods per plant were the factors that most significantly contributed to the overall divergence. Because of this, choosing superior genotypes based on these features may be crucial in breeding programs.

FUTURE SCOPE

The present investigation isolated the diverse clusters of genotypes. The genotypes with more genetic distance should be crossed to produce superior progeny. Hence our study provided the diverse genotype as parent to be utilized in future breeding program aimed at improving yield.

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Conflict of interest. None

REFERENCES

Anonymous, (2021). Directorate of Agriculture, Agriculture, Farmers welfare and co-operation development, Government of Gujarat. https://dag.gujarat.gov.in

Arora, R. N. and Pahuja, S. K. (2008). Mutagenesis in guar [*Cyamopsis tetragonoloba* (L.) Taub.]. *Plant Mutation Reports*, *2*(1): 7-9.

Ashraf, M. Y., Akhtar, K., Sarwar Gand, Ashraf, M. (2005). Role of the rooting system in salt tolerance potential of different guar accessions. *Agronomy Sustainable Development*, *25*: 243-249.

Bewal, S., Purohit, J., Kumar, A., Khedasana Rand, Rao, S. (2009). Cytogenetical investigations in colchicines induced tetraploids of [*Cyamopsis tetragonoloba* (L.) Taub.]. *Czech Journal of Genetics and Plant Breeding*, *45*: 143-154.

Bharodia, P. S., Zaveri, P. P., and Kher, H. R. (1993). GAUG 34 is a high yielding variety of clusterbean. *Indian Farm*, *43*(9): 31–33.

Bhatia, I. S., Nagpal, M. L., Singh, S. P., Kumar, N. A, Singh, M., and Parkash, O. (1979). Chemical nature of the pigment of the seed coat of guar [*Cyamopsis tetragonoloba* L. Taub.). *Journal of Agricultural Food Chemistry*, *27*(6): 1274-1276.

Bhosle, S. S., & Kothekar, V. S. (2010). Mutagenic efficiency and effectiveness in cluster bean (*Cyamopsis tetragonoloba* (L.) Taub.). *Journal of Phytology*, *2*(6), 21-27.

Chudzikowski, R. J. (1971). Guar gum and its applications. *Journal of the Society of Cosmetics Chemists*, *22*: 43-60.

Francois, L. E., Donovan, T. J. and Maas, E. V. (1990). Salinity effects on emergence, vegetative growth and seed yield of guar. *Agronomy Journal*, *82*: 587-592.

Gillette, J. B. (1958). Indigofera (Microcharis) in tropical Africa with the related genera *Cyamopsis* and *Rhyncotropis*. *Kew Bulletin Additional Series*, *1*: 1–66.

Henry, A., Daulay, H. S. and Bhati, T. K. (1992). Maru Guar promising clusterbean for arid region. *Indian Farm*. *42*(6): 24–25.

Hymowitz, T. and Matlock, R. S. (1963). Variations in seed coat colour of ‘groehler’ guar [*Cyamopsis tetragonolobus* (L.) Taub.] genetic or environmental. *Crop Sciences*, *1*(4): 65-69.

Kumar, S., Joshi, U. N., Singh, V., Singh, J. V., & Saini, M. L. (2013). Characterization of released and elite genotypes of guar [*Cyamopsis tetragonoloba* (L.) Taub.] from India proves unrelated to geographical origin. *Genetic resources and crop evolution*, *60*(7), 2017-2032.2032.

Mahalanobis, P. C. (1936). On the generalized distance in statistics. *Proceedings of National Academic Sciences*. *19*: 201-208.

Menon, U. (1973). A comparative review on crop improvement and utilization of clusterbean [*Cyamopsis tetragonoloba* (L.) Taub]. Department of Agriculture, Rajasthan, Jaipur. *Monographs Series*, *2*: 1–51.

Mishra, S. K., Singh, N. and Sharma, S. K. (2009). Status and utilization of genetic resources of arid legumes in India. In: Kumar D, Henry A (eds) Perspective research activities of arid legumes in India. *Indian Arid Legumes Society*, CAZRI, Jodhpur, pp. 23–30.

Ogwu, M. C., Osawaru, M. E. and Ahana, C. M. (2014). Challenges in conserving and utilizing plant genetic resources. *International Journal of Genetics and Molecular Biology*, *6*(2): 16–22.

Pathak, R., Singh, M. and Henry, A. (2010). Genetic divergence in clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.] for seed yield and gum content under rainfed conditions. *Indian Journal of Agricultural Sciences*, *79*(7): 559-61.

Rao, C. R. (1952). Advanced statistical methods in biometrical research. *Wiley and Sons*, New York.

Remzeena, A, Anitha, P. and Muhamed, S. (2018). Genetic divergence analysis in clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.]. *Legume Research-An International Journal*, *44*(3): 292-294.

Saini, M. L., Arora, R. N. and Paroda,R. S. (1981). Morphology of three species of genus *Cyamopsis*. *Guar Newsletter*, *2*: 7–11.

Shekhawat, S. S. and Choudhary, A. K. (2004). Quantitative genetic studies in clusterbean. In: Souvenir, *National Symposium on Arid Legumes for Sustainable Agriculture and Trade*, *5*: 3.

Siddaraju, R., Narayanaswamy, S., Ramegowda, and Prasad, S. R. (2010). Studies on growth, seed yield and yield attributes as influenced by varieties and row spacing in clusterbean [*Cyamopsis tetragonoloba* (L.) Taub.]. *Mysore Journal of Agricultural Sciences*, *44*: 16-21.

Undersander, D. J., Putnam, D. H., Kaminski, A. R., Kelling, K. A., Doll, J. D., Oplinger, E. S. and Gunsolus, J. L. (1991). *Guar: alternative field crops manual*. University of Wisconsin Extension.

Wankhade, R. S., Kale, V. S., Nagre, P. K. and Patil, R. K. (2017). Genetic divergence studies in cluster bean genotypes. *Legume Research*, *40*(5): 811-817.

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